



## RAW SEQUENCE LISTING

DATE: 04/01/2002

PATENT APPLICATION: US/08/994,468

TIME: 15:09:36

Input Set : N:\Crf3\RULE60\08994468.raw

Output Set: N:\CRF3\04012002\H994468.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

4 (i) APPLICANT: Lyman, Stewart D.

5 Beckmann, M. Patricia

7 (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

9 (iii) NUMBER OF SEQUENCES: 8

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation

13 (B) STREET: 51 University Street

14 (C) CITY: Seattle

15 (D) STATE: Washington

16 (E) COUNTRY: US

17 (F) ZIP: 98101

19 (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk

21 (B) COMPUTER: Apple Macintosh

22 (C) OPERATING SYSTEM: Macintosh 7.0.1

23 (D) SOFTWARE: Microsoft Word, Version #5.1

25 (vi) CURRENT APPLICATION DATA:

C--&gt; 26 (A) APPLICATION NUMBER: US/08/994,468

C--&gt; 27 (B) FILING DATE: 19-Dec-1997

48 (C) CLASSIFICATION:

45 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: 08/162,407

32 (B) FILING DATE:

36 (A) APPLICATION NUMBER: 08/111,758

37 (B) FILING DATE: August 25, 1993

41 (A) APPLICATION NUMBER: 08/106,463

42 (B) FILING DATE: August 12, 1993

46 (A) APPLICATION NUMBER: 08/068,394

47 (B) FILING DATE: May 24, 1993

50 (viii) ATTORNEY/AGENT INFORMATION:

51 (A) NAME: Malaska, Stephen L.

52 (B) REGISTRATION NUMBER: 32,655

53 (C) REFERENCE/DOCKET NUMBER: 2813-C

55 (ix) TELECOMMUNICATION INFORMATION:

56 (A) TELEPHONE: (206) 587-0430

57 (B) TELEFAX: (206) 233-0644

58 (C) TELEX: 756822

60 (2) INFORMATION FOR SEQ ID NO: 1:

62 (i) SEQUENCE CHARACTERISTICS:

63 (A) LENGTH: 879 base pairs

64 (B) TYPE: nucleic acid

ENTERED

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65         (C) STRANDEDNESS: single
66         (D) TOPOLOGY: linear
68         (ii) MOLECULE TYPE: cDNA to mRNA
70         (iii) HYPOTHETICAL: NO
72         (iv) ANTI-SENSE: NO
74         (ix) FEATURE:
75             (A) NAME/KEY: misc_feature
76             (B) LOCATION: 1..25
78         (ix) FEATURE:
79             (A) NAME/KEY: misc_feature
80             (B) LOCATION: 855..879
82         (ix) FEATURE:
83             (A) NAME/KEY: CDS
84             (B) LOCATION: 57..752
87         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
89 GTCGACTGGA ACGAGACGAC CTGCTCTGTC ACAGGCATGA GGGGTCCCCG GCAGAG      56
91 ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG CTG      104
92 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
93 1          5          10          15
95 CTG TTG CTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT TAC      152
96 Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
97          20          25          30
98 TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA GAG      200
99 Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
100         35          40          45
102 TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC AAT      248
103 Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
104         50          55          60
106 CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA GCC      296
107 Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
108 65          70          75          80
110 CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG ATG CAA      344
111 Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
112          85          90          95
114 ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA TGT      392
115 Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
116         100         105         110
118 ACC TTC CAG CCC CTA CCA GAA TGT CTG CGA TTC GTC CAG ACC AAC ATC      440
119 Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
120         115         120         125
122 TCC CAC CTC CTG AAG GAC ACC TGC ACA CAG CTG CTT GCT CTG AAG CCC      488
123 Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
124         130         135         140
126 TGT ATC GGG AAG GCC TGC CAG AAT TTC TCT CGG TGC CTG GAG GTG CAG      536
127 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
128 145         150         155         160
130 TGC CAG CCG GAC TCC TCC ACC CTG CTG CCC CCA AGG AGT CCC ATA GCC      584
131 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
132         165         170         175

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134 CTA GAA GCC ACG GAG CTC CCA GAG CCT CGG CCC AGG CAG CTG TTG CTC      632
135 Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
136              180              185              190
138 CTG CTG CTG CTG CTG CCT CTC ACA CTG GTG CTG CTG GCA GCC GCC TGG      680
139 Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
140              195              200              205
142 GGC CTT CGC TGG CAA AGG GCA AGA AGG AGG GGG GAG CTC CAC CCT GGG      728
143 Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
144              210              215              220
146 GTG CCC CTC CCC TCC CAT CCC TAGGATTCGA GCCTTGTCGA TCGTTGACTC      779
147 Val Pro Leu Pro Ser His Pro
148 225              230
150 AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC AGAGCAGGAT 839
152 TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC      879
154 (2) INFORMATION FOR SEQ ID NO: 2:
156     (i) SEQUENCE CHARACTERISTICS:
157         (A) LENGTH: 231 amino acids
158         (B) TYPE: amino acid
159         (D) TOPOLOGY: linear
161     (ii) MOLECULE TYPE: protein
164     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
166 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
167  1              5              10              15
169 Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
170              20              25              30
172 Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
173              35              40              45
175 Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
176              50              55              60
178 Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
179 65              70              75              80
181 Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
182              85              90              95
184 Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
185              100             105             110
187 Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
188              115             120             125
190 Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
191              130             135             140
193 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
194 145             150             155             160
196 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
197              165             170             175
199 Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
200              180             185             190
202 Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
203              195             200             205
205 Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
206              210             215             220

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208 Val Pro Leu Pro Ser His Pro
209 225                230
211 (2) INFORMATION FOR SEQ ID NO: 3:
213     (i) SEQUENCE CHARACTERISTICS:
214         (A) LENGTH: 24 base pairs
215         (B) TYPE: nucleic acid
216         (C) STRANDEDNESS: single
217         (D) TOPOLOGY: linear
219     (iii) HYPOTHETICAL: NO
221     (iv) ANTI-SENSE: NO
223     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
225 TCGACTGGAA CGAGACGACC TGCT                24
228 (2) INFORMATION FOR SEQ ID NO: 4:
230     (i) SEQUENCE CHARACTERISTICS:
231         (A) LENGTH: 20 base pairs
232         (B) TYPE: nucleic acid
233         (C) STRANDEDNESS: single
234         (D) TOPOLOGY: linear
236     (iii) HYPOTHETICAL: NO
238     (iv) ANTI-SENSE: NO
240     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
242 AGCAGGTCGT CTCGTTCCAG                20
244 (2) INFORMATION FOR SEQ ID NO: 5:
246     (i) SEQUENCE CHARACTERISTICS:
247         (A) LENGTH: 988 base pairs
248         (B) TYPE: nucleic acid
249         (C) STRANDEDNESS: single
250         (D) TOPOLOGY: linear
252     (ii) MOLECULE TYPE: cDNA to mRNA
254     (iii) HYPOTHETICAL: NO
256     (iv) ANTI-SENSE: NO
258     (ix) FEATURE:
259         (A) NAME/KEY: CDS
260         (B) LOCATION: 30..734
262     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
264 CGGCCGGAAT TCCGGGGCCC CCGGCCGAA ATG ACA GTG CTG GCG CCA GCC TGG    53
265                               Met Thr Val Leu Ala Pro Ala Trp
266                               1           5
268 AGC CCA ACA ACC TAT CTC CTC CTG CTG CTG CTG AGC TCG GGA CTC    101
269 Ser Pro Thr Thr Tyr Leu Leu Leu Leu Leu Leu Ser Ser Gly Leu
270 10           15           20
272 AGT GGG ACC CAG GAC TGC TCC TTC CAA CAC AGC CCC ATC TCC TCC GAC    149
273 Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
274 25           30           35           40
276 TTC GCT GTC AAA ATC CGT GAG CTG TCT GAC TAC CTG CTT CAA GAT TAC    197
277 Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
278           45           50           55
280 CCA GTC ACC GTG GCC TCC AAC CTG CAG GAC GAG GAG CTC TGC GGG GGC    245
281 Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly

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282          60          65          70
284 CTC TGG CGG CTG GTC CTG GCA CAG CGC TGG ATG GAG CGG CTC AAG ACT 293
285 Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
286          75          80          85
288 GTC GCT GGG TCC AAG ATG CAA GGC TTG CTG GAG CGC GTG AAC ACG GAG 341
289 Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu
290          90          95          100
292 ATA CAC TTT GTC ACC AAA TGT GCC TTT CAG CCC CCC CCC AGC TGT CTT 389
293 Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Ser Cys Leu
294 105          110          115          120
296 CGC TTC GTC CAG ACC AAC ATC TCC CGC CTC CTG CAG GAG ACC TCC GAG 437
297 Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu
298          125          130          135
300 CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC CGG 485
301 Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg
302          140          145          150
304 TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC CCA 533
305 Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro
306          155          160          165
308 TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC 581
309 Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro
310          170          175          180
312 CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC 629
313 Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala
314 185          190          195          200
316 GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC 677
317 Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg
318          205          210          215
320 CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT 725
321 Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu
322          220          225          230
324 GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC 774
325 Val Glu His
326          235
328 GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG GATACTGAGG CACACAGAGG 834
330 GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC 894
332 CCTTCCTTGG GCCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC 954
334 GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCC 988
336 (2) INFORMATION FOR SEQ ID NO: 6:
338 (i) SEQUENCE CHARACTERISTICS:
339 (A) LENGTH: 235 amino acids
340 (B) TYPE: amino acid
341 (D) TOPOLOGY: linear
343 (ii) MOLECULE TYPE: protein
345 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
347 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
348 1 5 10 15
350 Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
351 20 25 30

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## VERIFICATION SUMMARY

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L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]